

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA  
COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
GORDON, JULIAN  
GRANADOS, EDWARD N.  
HODGES, STEVEN C.  
KLASS, MICHAEL R.  
KRATOCHVIL, JON D.  
RUSSELL, JOHN C.  
SCHEFFEL, CHRISTI  
STROUPE, STEPHEN D.  
YU, HONG

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE BREAST

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Road  
(C) CITY: Abbott Park  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/879,354  
(B) FILING DATE: 20-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.  
(B) REGISTRATION NUMBER: 35,441  
(C) REFERENCE/DOCKET NUMBER: 6120.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729  
(B) TELEFAX: 847/938-2623  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACGCCCAGT	GACCTGCCGA	GGTCGGCAGC	ACAGAGCTCT	GGAGATGAAG	ACCCTGTTCC	60
TGGGTGTCAC	GCTCGGCCTG	GCCGCTGCCC	TGTCCTTCAC	CCTGGAGGAG	GAGGATATCA	120
CAGGGACCTG	GTACGTGAAG	GCCATGGTGG	TCGATAAGGA	CTTTCCGGAG	GACAGGAGGC	180
CCAGGAAGGT	GTCCCCAGTG	AAGGTGACAG	CCCTGGGCGG	TGGGAAGTTG	GAAGCC	236

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATATCACA	GGGACCTGGT	ACGTGAAGGC	CATGGTGGTC	GATAAGGACT	TTCCGGAGGA	60
CAGGAGGCCC	AGGAAGGTGT	CCCCAGTGAA	GGTGACAGCC	CTGGGCGGTG	GGAAGTTGGA	120
AGCCACGTTT	ACCTTCATGA	GGGAGGATCG	GTGCATCCAG	AAGAAAATCC	TGATGCGGAA	180
GACGGAGGAG	CCTGGCAAAT	ACAGCGCCTA	TGGGGGCAGG	AAGCTCATGT	ACCTGCAGGA	240
GCTGC						245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGGGAGAAG	GACTTTATTT	GGAGTCAGGT	GGGTGGGAGC	AGGGAAGGGT	CATGGCTGGA	60
GGGTAGGTCC	AGGTGGTCCG	GGCTCTGTGT	CTGGTGGTAG	GGTGGGCTCT	GGAGGTGCAG	120
ACCCGGGGGC	TGCCTAGTGT	TCGGGAACGC	AGCTTCCCCT	CTGCAGGGGC	GTGAAAATGT	180
CCTCCTCCGA	GAGTCCCTTG	CGCTGCACCA	ATTCTTAAA	TTCTTCCAGG	GCCTCCCGGT	240
TGGTATCAGA	ATTCTACCC	ACAAGCTTTC	CCATGTGGAG	CAGGCCCCCA	TGGTGCTGGT	300
CTTTGCAGTA	AAAGATGTAG	TGGTCCCTCC	TGGGCAG			337

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACGCCCAGT	GACCTGCCGA	GGTCGGCAGC	ACAGAGCTCT	GGAGATGAAG	ACCCTGTTCC	60
TGGGTGTCAC	GCTCGGCCTG	GCCGCTGCCC	TGTCCTTCAC	CCTGGAGGAG	GAGGATATCA	120
CAGGGACCTG	GTACGTGAAG	GCCATGGTGG	TCGATAAGGA	CTTTCCGGAG	GACAGGAGGC	180
CCAGGAAGGT	GTCCCCAGTG	AAGGTGACAG	CCCTGGGCGG	TGGGAAGTTG	GAAGCCACGT	240

Seq 1 2 3 4

TCACCTTCAT	GAGGGAGGAT	CGGTGCATCC	AGAAGAAAAT	CCTGATGCGG	AAGACGGAGG	300
AGCCTGGCAA	ATACAGCGCC	TATGGGGGCA	GGAAGCTCAT	GTACCTGCAG	GAGCTGCCCA	360
GGAGGGACCA	CTACATCTTT	TACTGCAAAG	ACCAGCACCA	TGGGGGCGTG	CTCCACATGG	420
GAAAGCTTGT	GGGTAGGAAT	TCTGATACCA	ACCGGGAGGC	CCTGGAAGAA	TTTAAGAAAT	480
TGGTGCAGCG	CAAGGGACTC	TCGGAGGAGG	ACATTTTCAC	GCCCCTGCAG	ACGGGAAGCT	540
GCGTTCCCCG	ACACTAGGCA	GCCCCCGGGT	CTGCACCTCC	AGAGCCCACC	CTACCACCAG	600
ACACAGAGCC	CGGACCACCT	GGACCTACCC	TCCAGCCATG	ACCCTTCCCT	GCTCCCACCC	660
ACCTGACTCC	AAATAAAGTC	CTTCTCCCCC	CA			692

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGCCCAGT	GACCTGCCGA	GGTCGGCAGC	ACAGAGCTCT	GGAGATGAAG	ACCCTGTTCC	60
TGGGTGTCAC	GCTCGGCCTG	GCCGCTGCCC	TGTCCTTCAC	CCTGGAGGAG	GAGGATATCA	120
CAGGGACCTG	GTACGTGAAG	GCCATGGTGG	TCGATAAGGA	CTTCCGGAG	GACAGGAGGC	180
CCAGGAAGGT	GTCCCCAGTG	AAGGTGACAG	CCCTGGGCGG	TGGGAAGTTG	GAAGCCACGT	240
TCACCTTCAT	GAGGGAGGAT	CGGTGCATCC	AGAAGAAAAT	CCTGATGCGG	AAGACGGAGG	300
AGCCTGGCAA	ATACAGCGCC	TATGGGGGCA	GGAAGCTCAT	GTACCTGCAG	GAGCTGCCCA	360
GGAGGGACCA	CTACATCTTT	TACTGCAAAG	ACCAGACCA	TGGGGGCGTG	CTCCACATGG	420
GAAAGCTTGT	GGGTAGGAAT	TCTGATACCA	ACCGGGAGGC	CCTGGAAGAA	TTTAAGAAAT	480
TGGTGCAGCG	CAAGGGACTC	TCGGAGGAGG	ACATTTTCAC	GCCCCTGCAG	ACGGGAAGCT	540
GCGTTCCCCG	ACACTAGGCA	GCCCCCGGGT	CTGCACCTCC	AGAGCCCACC	CTACCACCAG	600
ACACAGAGCC	CGGACCACCT	GGACCTACCC	TCCAGCCATG	ACCCTTCCCT	GCTCCCACCC	660
ACCTGACTCC	AAATAAAGTC	CTTCTCCCCC	CA			692

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAATGTCCT CCTCCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTTTTTTT TTTTTTTTTT TTTTGT

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTTGGAAGC CACGTTTAC

19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCATAGGCG CTGTATTGT

19

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGTTGGAAGC CACGTTTAC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGCTGGT CTTTGCAGTA AAAG

24

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAATACAGC GCCTA

15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCCAATCAGC ACGTTGTAAA ACG

23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGGCCGCCG TGTTCCGGAA CGCAGCTT

28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Lys	Thr	Leu	Phe	Leu	Gly	Val	Thr	Leu	Gly	Leu	Ala	Ala	Ala	Leu
1				5					10					15	
Ser	Phe	Thr	Leu	Glu	Glu	Glu	Asp	Ile	Thr	Gly	Thr	Trp	Tyr	Val	Lys
			20					25					30		
Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	Pro	Arg	Lys
		35					40					45			
Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly	Lys	Leu	Glu	Ala
		50				55					60				

Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile	Gln	Lys	Lys	Ile	Leu
65					70					75					80
Met	Arg	Lys	Thr	Glu	Pro	Gly	Lys	Tyr	Ser	Ala	Tyr	Gly	Gly	Arg	
				85				90					95		
Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	Arg	Arg	Asp	His	Tyr	Ile	Phe
			100					105				110			
Tyr	Cys	Lys	Asp	Gln	His	His	Gly	Gly	Leu	Leu	His	Met	Gly	Lys	Leu
		115					120					125			
Val	Gly	Arg	Asn	Ser	Asp	Thr	Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys
	130					135					140				
Lys	Leu	Val	Gln	Arg	Lys	Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro
145					150					155					160
Leu	Gln	Thr	Gly	Ser	Cys	Val	Pro	Glu	His						
				165					170						

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu	Glu	Glu	Glu	Asp	Ile	Thr	Gly	Thr	Trp	Tyr	Val	Lys	Ala	Met	Val
1				5					10					15	
Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	Pro	Arg	Lys	Val	Ser	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly	Lys	Leu	Glu	Ala	Thr	Phe
1				5					10					15	
Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile	Gln	Lys	Lys				
			20					25							

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	Ser	Ala	Tyr	Gly
1				5					10					15	
Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu						
			20					25							

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His  
1 5 10 15  
His His His His His  
20